

1642

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/068,377A

DATE: 02/22/2001
 TIME: 10:34:23

Input Set : A:\PTO.txt
 Output Set: N:\CRF3\02222001\I068377A.raw

RECEIVED

MAR 01 2001

TECH CENTER 1600/2900

Does Not Comply
 Corrected Diskette Needed

See pp. 2-9

3 <110> APPLICANT: Lasky, Laurence A.
 4 Dowbenko, Donald J.
 6 <120> TITLE OF INVENTION: Tyrosine Phosphorylated Cleavage Furrow-Associated
 7 Proteins (PSTPIPs)
 9 <130> FILE REFERENCE: P1066P2
 11 <140> CURRENT APPLICATION NUMBER: US 09/068,377A
 12 <141> CURRENT FILING DATE: 1998-05-08
 14 <150> PRIOR APPLICATION NUMBER: PCT/US98/01774
 15 <151> PRIOR FILING DATE: 1998-01-30
 17 <150> PRIOR APPLICATION NUMBER: US 08/938,830
 18 <151> PRIOR FILING DATE: 1997-09-29
 20 <150> PRIOR APPLICATION NUMBER: US 08/798,419
 21 <151> PRIOR FILING DATE: 1997-02-07
 E--> 23 <160> NUMBER OF SEQ ID NOS: 73

ERRORED SEQUENCES

510 <210> SEQ ID NO: 26
 511 <211> LENGTH: 907
 512 <212> TYPE: PRT
 513 <213> ORGANISM: Saccharomyces Pombe
 515 <400> SEQUENCE: 26
 516 Met Leu Thr Lys Ser Leu Gln Gly Ser Glu Asp Ala Gly Met Asp
 517 1 5 10 15
 519 Ala Leu Met Ser Arg Thr Lys Ser Ser Leu Ser Val Leu Glu Ser
 520 20 25 30
 522 Ile Asp Glu Phe Tyr Ala Lys Arg Ala Ser Ile Glu Arg Glu Tyr
 523 35 40 45
 525 Ala Ser Lys Leu Gln Glu Leu Ala Ala Ser Ser Ala Asp Ile Pro
 526 50 55 60
 528 Glu Val Gly Ser Thr Leu Asn Asn Ile Leu Ser Met Arg Thr Glu
 529 65 70 75
 531 Thr Gly Ser Met Ala Lys Ala His Glu Glu Val Ser Gln Gln Ile
 532 80 85 90
 534 Asn Thr Glu Leu Arg Asn Lys Ile Arg Glu Tyr Ile Asp Gln Thr
 535 95 100 105
 537 Glu Gln Gln Lys Val Val Ala Ala Asn Ala Ile Glu Glu Leu Tyr
 538 110 115 120
 540 Gln Lys Lys Thr Ala Leu Glu Ile Asp Leu Ser Glu Lys Lys Asp
 541 125 130 135
 543 Ala Tyr Glu Tyr Ser Cys Asn Lys Leu Asn Ser Tyr Met Arg Gln
 544 140 145 150
 546 Thr Lys Lys Met Thr Gly Arg Glu Leu Asp Lys Tyr Asn Leu Lys
 547 155 160 165
 549 Ile Arg Gln Ala Ala Leu Ala Val Lys Lys Met Asp Ala Glu Tyr
 550 170 175 180

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```

552 Arg Glu Thr Asn Glu Leu Leu Leu Thr Val Thr Arg Glu Trp Ile
553                               185                               190                               195
555 Asp Arg Trp Thr Glu Val Cys Asp Ala Phe Gln His Ile Glu Glu
556                               200                               205                               210
558 Tyr Arg Leu Glu Phe Leu Lys Thr Asn Met Trp Ala Tyr Ala Asn
559                               215                               220                               225
561 Ile Ile Ser Thr Ala Cys Val Lys Asp Asp Glu Ser Cys Glu Lys
562                               230                               235                               240
564 Ile Arg Leu Thr Leu Glu Asn Thr Asn Ile Asp Glu Asp Ile Thr
565                               245                               250                               255
567 Gln Met Ile Gln Asn Glu Gly Thr Gly Thr Thr Ile Pro Pro Leu
568                               260                               265                               270
570 Pro Glu Phe Asn Asp Tyr Phe Lys Glu Asn Gly Leu Asn Tyr Asp
571                               275                               280                               285
573 Ile Asp Gln Leu Ile Ser Lys Ala Pro Ser Tyr Pro Tyr Ser Ser
574                               290                               295                               300
576 Ser Arg Pro Ser Ala Ser Ala Ser Leu Ala Ser Ser Pro Thr Arg
577                               305                               310                               315
579 Ser Ala Phe Arg Pro Lys Thr Ser Glu Thr Val Ser Ser Glu Val
580                               320                               325                               330
582 Val Ser Ser Pro Pro Thr Ser Pro Leu His Ser Pro Val Lys Pro
583                               335                               340                               345
585 Val Ser Asn Glu Gln Val Glu Gln Val Thr Glu Val Glu Leu Ser
586                               350                               355                               360
588 Ile Pro Val Pro Ser Ile Gln Glu Ala Glu Ser Gln Lys Pro Val
589                               365                               370                               375
591 Leu Thr Gly Ser Ser Met Arg Arg Pro Ser Val Thr Ser Pro Thr
592                               380                               385                               390
594 Phe Glu Val Ala Ala Arg Pro Leu Thr Ser Met Asp Val Arg Ser
595                               395                               400                               405
597 Ser His Asn Ala Glu Thr Glu Val Gln Ala Ile Pro Ala Ala Thr
598                               410                               415                               420
600 Asp Ile Ser Pro Glu Val Lys Glu Gly Lys Asn Ser Glu Asn Ala
601                               425                               430                               435
603 Ile Thr Lys Asp Asn Asp Asp Ile Ile Leu Ser Ser Gln Leu Gln
604                               440                               445                               450
606 Pro Thr Ala Thr Gly Ser Arg Ser Ser Arg Leu Ser Phe Ser Arg
607                               455                               460                               465
609 His Gly His Gly Ser Gln Thr Ser Leu Gly Ser Ile Lys Arg Lys
610                               470                               475                               480
612 Ser Ile Met Glu Arg Met Gly Arg Pro Thr Ser Pro Phe Met Gly
613                               485                               490                               495

```

```

615 Ser Ser Phe Ser
E--> 616 Asn????????????????????????????????????????????????????????????????????????????????????
E--> 617 ?????????????????????????????????????????????????????????????????tgaagcagc aa 42
E--> 619 <210> SEQ ID NO: 33
620 <211> LENGTH: 42
621 <212> TYPE: DNA
622 <213> ORGANISM: Artificial Sequence

```

*Indicates possible
bad disk sector.*

RAW SEQUENCE LISTING DATE: 02/22/2001
PATENT APPLICATION: US/09/068,377A TIME: 10:34:23

Input Set : A:\PTO.txt
Output Set: N:\CRF3\02222001\I068377A.raw

```
624 <220> FEATURE:
625 <223> OTHER INFORMATION: Synthetic oligonucleotide probe
627        628        ?????????????????????????????????????????????????????????
629 <223> OTHER INFORMATION: Synthetic oligonucleotide probe
E--> 631 <400> SEQUENCE: 34
632    cagttcggat ccatgatggt ccagaagagc aagttgtcgc tc 42
E--> 634 <210> SEQ ID NO: 35
635 <211> LENGTH: 42
W--> 640 <212> TYPE:
W--> 640 <213> ORGANISM:
E--> 640 <400> SEQUENCE: 37
641    ttgacctcga gtcatacccg ctcaggggtg ggagtcagag tc 42
E--> 643 <210> SEQ ID NO: 38
644 <211> LENGTH: 40
E--> 645 <212> TYPE:
649 <210> SEQ ID NO: 39
W--> 650 <211> LENGTH: 45
W--> 651 <212> TYPE: DNA
652 <213> ORGANISM: Artificial Sequence
654 <220> FEATURE:
655 <223> OTHER INFORMATION: Synthetic oligonucleotide probe
E--> 657 <400> SEQUENCE: 37
658    ?????????????????????????????????????????????????????????????????????
659    ?????????????????????????????????????????????????????????tggtta cagtcaccc acagggca 48
E--> 661 <210> SEQ ID NO: 42
662 <211> LENGTH: 47
663 <212> TYPE: DNA
664 <213> ORGANISM: Artificial Sequence
666 <220> FEATURE:
667 <223> OTHER INFORMATION: Synthetic
668    Oligonucleot????????????????????????????????????????????????????????
669    ?????????????????????????????????????????????????????????????????1 Sequence
671 <220> FEATURE:
672 <223> OTHER INFORMATION: Synthetic oligonucleotide probe
E--> 674 <400> SEQUENCE: 43
E--> 675    gtctgaggag ctccgccgca gccttgac 29
E--> 677 <210> SEQ ID NO: 44
678 <211> LENGTH:
W--> 682 <212> TYPE:
W--> 682 <213> ORGANISM:
E--> 682 <400> SEQUENCE: 46
683    caggagatca aaggcgccg ccaggagatt catc 34
E--> 685 <210> SEQ ID NO: 47
686 <211> LENGTH: 34
687 <212> TYPE: DNA
W--> 688 <213> ORGANISM:
W--> 691 <211> LENGTH: 37
W--> 692 <212> TYPE: DNA
```

possible bad disk sector

RAW SEQUENCE LISTING DATE: 02/22/2001
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Input Set : A:\PTO.txt
Output Set: N:\CRF3\02222001\I068377A.raw

W--> 693 <213> ORGANISM: Artificial Sequence
695 <220> FEATURE:
696 <223> OTHER INFORMATION: Synthetic oligonucleotide probe
E--> 698 <400> SEQUENCE: 48
E--> 699 cctccaagct
W--> 700 tgcga??
E--> 701 ???DNA
W--> 702 <213> ORGANISM: Artificial Sequence
704 <220> FEATURE:
705 <223> OTHER INFORMATION: Synthetic oligonucleotide probe
W--> 707 <210> SEQ ID NO:
W--> 707 <211> LENGTH:
W--> 707 <212> TYPE:
E--> 707 <400> SEQUENCE: 51
E--> 708 ggtcttcttg gcggcgcga gcttgctctt
W--> 709 ct??
E--> 710 ???atccctgc acgcgcgcgc atataagctt
711 tcttggaact ca 42
E--> 713 <210> SEQ ID NO: 53
E--> 724 <210> SEQ ID NO: 56
W--> 725 <211> LENGTH: 31
W--> 726 <212> TYPE: DNA
W--> 727 <213> ORGANISM: Artificial Sequence
729 <220> FEATURE:
E--> 730 ???
733 <220> FEATURE:
734 <223> OTHER INFORMATION: Synthetic oligonucleotide probe
E--> 736 <400> SEQUENCE: 57
737 ggatggtgag cgggtctgcc tctgcagct ggaggcc 37
W--> 739 ???
E--> 740 ??? Sequence
742 <220> FEATURE:
743 <223> OTHER INFORMATION: Synthetic oligonucleotide probe
W--> 745 <210> SEQ ID NO:
W--> 745 <211> LENGTH:
W--> 745 <212> TYPE:
W--> 745 <213> ORGANISM:
E--> 745 <400> SEQUENCE: 60
746 tccacatcct tggacatctt cctg 24
E--> 748 <210> SEQ ID NO: 61
749 <211> LENGTH: 41
E--> 750 <21??
753 <210> SEQ ID NO: 62
W--> 754 <211> LENGTH: 24
755 <212> TYPE: DNA
756 <213> ORGANISM: Artificial Sequence
758 <220> FEATURE:
759 <223> OTHER INFORMATION: Synthetic oligonucleotide probe
761 ???

Bad disk sector

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Input Set : A:\PTO.txt
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```
762      ?????????????????????????????????????????????????????????
W--> 763 <213> ORGANISM: Artificial Sequence
765 <220> FEATURE:
766 <223> OTHER INFORMATION: Synthetic oligonucleotide probe
E--> 768 <400> SEQUENCE: 65
769   catcatcctt gacggactgc atggagagct 30
W--> 770 ?????????????????????????????????????????????????????????
W--> 771 ?????????????????????????????????????????????????????ct tccacatcgg agccctcaag ggtcag
E--> 772 36
E--> 774 <210> SEQ ID NO: 67
E--> 784 <210> SEQ ID NO: 70
W--> 785 <211> LENGTH: 30
W--> 786 <212> TYPE: DNA
W--> 787 <213> ORGANISM: Artificial Sequence
789 <220> FEATURE:
790 <223> OTHER INFORMATION: Synthetic oligonucleotide probe
E--> 792 <400> SEQUENCE: 65
W--> 793 70????????????????????????????????????????????????????????
E--> 794 ?????????????????????????????????????????????????onucleotide probe
W--> 796 <210> SEQ ID NO:
W--> 796 <211> LENGTH:
W--> 796 <212> TYPE:
W--> 796 <213> ORGANISM:
E--> 796 <400> SEQUENCE: 71
W--> 797   ctgcaggagg atccgcgggc cctttgggcc ttcc 34
E--> 799 <210> SEQ ID NO: 72
800 <211> LENGTH: 31
801 <212> TYPE: DNA
802 <213> ORGANISM: Artificial
W--> 818 <130> FILE REFERENCE: P1066P2
W--> 818 <130> FILE REFERENCE: P1066P2
W--> 820 <140> CURRENT APPLICATION NUMBER: US 09/068,377A
821 <141> CURRENT FILING DATE: 1998-05-08
W--> 823 <150> PRIOR APPLICATION NUMBER:
828   Ala Arg Lys Ala Gly Gly Gln Thr Glu Met Asn Ser Leu Arg Thr
W--> 830 ?????????????????????????????????????????????????????????
E--> 831 ?????????????????????????????????????????????????      80      85
E--> 832 90
834   His Ile Gln Leu Ala Leu Ala Leu Arg Glu Glu Leu Arg Ser Leu
W--> 836 ?????????????????????????????????????????????????????????
E--> 837 ?????????????????????????????????????????????????      145
E--> 838 150
840   Ala Asp Asp Ala Glu Gln Ala Phe Glu Arg Val Ser Ala Asn Gly
W--> 841      155
W--> 842 ?????????????????????????????????????????????????????????
E--> 843 ?????????????????????????????????????????????????      175
E--> 844 180
846   Lys Glu Ser Ala Thr Glu Ala Glu Arg Val Tyr Arg Gln Asn Ile
W--> 847      185
```

Same

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Input Set : A:\PTO.txt
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```
W--> 848 ?????????????????????????????????????????????????????????????
E--> 849 ????????????????????????????????????????????????????????????? 235 240
      851 Gln Cys Val Lys Asp Asp Glu Leu Tyr Glu Glu Val Arg Leu Thr
W--> 852 245
W--> 853 ?????????????????????????????????????????????????????????????
E--> 854 ????????????????????????????????????????????????????????????? 265 270
      856 Ser Lys Ser Thr Gly Arg Glu Pro Pro Ala Pro Val Pro Tyr Gln
W--> 857 275
W--> 858 28????????????????????????????????????????????????????????????
E--> 859 ????????????????????????????????????????????????????????????? 330
      861 Glu Thr Leu Thr Pro Thr Pro Glu Arg Asn Glu Leu Val Tyr Ala
W--> 862 335 340
W--> 863 ?????????????????????????????????????????????????????????????
E--> 864 ????????????????????????????????????????????????????????????? 360
      866 Gln Asp Tyr Arg Ala Leu Tyr Asp Tyr Thr Ala Gln Asn Ser Asp
W--> 867 365 370
E--> 868 ?????????????????????????????????????????????????????????????
W--> 869 <213> ORGANISM: Mus Musculus
E--> 871 <400> SEQUENCE: 2
      872 caatatattca agctataacca agcatacaat caactccaag cttatgccca 50
E--> 874 agaagaagcg gaaggtctcg agcggcgcca
E--> 875 at????????????????????????????????????????????????????????????
E--> 876 ?????????????????????????????????????????????????????ctttca caaccaattg 200
E--> 878 cctcctctaa cggttcgatg aacttcgatga ataataaat cagggctagt 250
E--> 880 aaaattgatg atggtataaa ttcaaaacca
E--> 881 ctgtca????????????????????????????????????????????????????????????
E--> 882 ?????????????????????????????????????????????????????gctgggact 600
E--> 884 gggacgtgct cctggctcct ggcccatgct cagccctgct tgaagcagga 650
E--> 886 gtgctagcat ttgacacaac gccctggag gatgatggcc
W--> 887 cag????????????????????????????????????????????????????????????
E--> 888 ?????????????????????????????????????????????????????gtgga 800
E--> 890 ggagctgctc agacagaggg cccagggcga ggagaggtac gggaaggagc 850
E--> 892 tgggtgcagat tgcacgcaag gctggtggcc agacagagat
W--> 893 gaattcc????????????????????????????????????????????????????????????
E--> 894 ?????????????????????????????????????????????????????????c 1200
E--> 896 cagaacaaag ccaagcagtg caaggagtca gccacagagg cagaaagagt 1250
E--> 898 gtacaggcaa aatatcgaac aactggagag agcaggagacc
W--> 899 gaggggag????????????????????????????????????????????????????????????
E--> 900 ?????????????????????????????????????????????????????t 1400
E--> 902 gcagtgtgtc aaggatgatg agctctatga ggaagtgcgg ctgacccttg 1450
E--> 904 agggctgtga tgtggaagggt gacatcaatg gcttcattca
W--> 905 gtccaagag????????????????????????????????????????????????????????????
E--> 906 ?????????????????????????????????????????????????????t 1800
E--> 908 tctgatgagc tggacatttc cgcgggagac atcctggcgg tcatcctgga 1850
E--> 910 aggggaggat ggctggtgga ctgtggagcg gaacggacaa
W--> 911 cgtggcttt????????????????????????????????????????????????????????????
E--> 912 ?????????????????????????????????????????????????????c 2000
E--> 914 caggcctcac ggggacagaa ccaagcccg tgggtgctgg catgggctgg 2050
E--> 916 gtgctggcta ctctcaataa atgtctccca gaaggaaaaa
```

Same

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Input Set : A:\PTO.txt
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```
W--> 917 aaaaaaaaaa????????????????????????????????????????????????????????????
E--> 918 ?????????????????????????????????????????????????????????????
W--> 919                      35                      40                      45
E--> 921    Tyr Leu Arg
     924 <210> SEQ ID NO: 4
     925 <211> LENGTH: 50
     926 <212> TYPE: PRT
     927 <213> ORGANISM: Homo
     931 Val Asn Glu Val Ile Glu Ile Leu Ile Glu Asp Ser Ser Gly Trp
E--> 932                      20                      25
E--> 933 ?????????????????????????????????????????????????????????????
E--> 934 ?????????????????????????????????????????????????????????????e Leu Thr Leu Leu Asn Ser Thr
E--> 935 Asn Lys Asp Trp
E--> 936                      20                      25                      30
     938 Trp Lys Val Glu
E--> 939 ?????????????????????????????????????????????????????????????
E--> 940 ?????????????????????????????????????????????????????????????u
E--> 941                      50
E--> 943 <210> SEQ ID NO: 6
W--> 944 <211> LENGTH: 50
W--> 945 <212> TYPE: PRT
W--> 946 <213> ORGANISM: Homo sapien
     948 <400> SEQUENCE: 6
     949 Leu Tyr Asp Tyr Gln Gly Glu Gly Ser Asp
E--> 950 ?????????????????????????????????????????????????????????????
     951 <210> SEQ ID NO: 7
     952 <211> LENGTH: 48
     953 <212> TYPE: PRT
     954 <213> ORGANISM: Homo sapien
     956 <400> SEQUENCE: 7
     957 Leu Tyr Asp Tyr Gln Ala Ala Gly Asp Asp Glu Ile Ser Phe Asp
E--> 958    1
E--> 959 ?????????????????????????????????????????????????????????????
     960 ?????????????????????????????????????????????????????????????                    20                      25
E--> 961 30
     963 Trp Arg Gly Val Cys Lys Gly Arg Tyr Gly Leu Phe Pro Ala Asn
E--> 965 ?????????????????????????????????????????????????????????????
E--> 966 ???????????????????????????????????????????????????????????? ttc 33
E--> 968 <210> SEQ ID NO: 10
     969 <211> LENGTH: 45
     970 <212> TYPE: DNA
     971 <213> ORGANISM: Artificial Sequence
     973 <220> FEATURE:
     974 <223> OTHER INFORMATION: Synthetic oligonucleotide probe
E--> 976 <400> SEQUENCE: 7
W--> 977 10????????????????????????????????????????????????????????????
W--> 978 ????????????????????????????????????????????????????????????3> Synthetic oligonucleotide
E--> 979 probe
W--> 981 <210> SEQ ID NO:
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Same

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W--> 981 <211> LENGTH:
W--> 981 <212> TYPE:
W--> 981 <213> ORGANISM:
E--> 981 <400> SEQUENCE: 11
W--> 982 tgcctttctc tccacagg 18
E--> 984 <210> SEQ ID NO: 12
985 <211> LENGTH: 36
986 <212> TYPE: DNA
987 <213> ORGANISM: Artificial
E--> 991 <400> SEQUENCE: 14
E--> 992 gcgtttggaa tcactac 17
E--> 994 <210> SEQ ID NO: 15
995 <211> LENGTH: 41
996 <212> TYPE: DNA
997 <213> ORGANISM: Artificial Sequence
999 <220> FEATURE:
1000 <223> OTHER INFORMATION: Synthetic
1001 oligo???
1002 ??al Sequence
1004 <220> FEATURE:
1005 <223> OTHER INFORMATION: Synthetic oligonucleotide probe
E--> 1007 <400> SEQUENCE: 16
E--> 1008 gtacgcgtcg accgcactct acgactacac tgcacag 37
E--> 1010 <210> SEQ ID NO:
W--> 1014 <211> LENGTH:
W--> 1014 <212> TYPE:
W--> 1014 <213> ORGANISM:
E--> 1014 <400> SEQUENCE: 19
1015 gatcctcgag ttacaccogt gtccactctg ctggagga 38
1017 <210> SEQ ID NO: 20
1018 <211> LENGTH: 20
1019 <212> TYPE: PRT
W--> 1020 <213> ORGANISM:
1025 Pro Ala Glu Trp Thr
E--> 1026 20
1028 <210> SEQ ID NO: 21
W--> 1029 <211> LENGTH: 19
E--> 1030 <2???
W--> 1044 <213> ORGANISM: Saccharomyces Pombe
E--> 1046 <400> SEQUENCE: 26
1047 Met Leu Thr Lys Ser Leu Gln GlySer Glu Asp Ala Gly Met Asp
E--> 1048 1
E--> 1049 5???
1050 ?? 25
E--> 1051 30
1053 Ile Asp Glu Phe Tyr Ala Lys Arg Ala Ser Ile Glu Arg Glu Tyr
E--> 1054 35
E--> 1055 ??
1056 ?? 85 90

Same

VERIFICATION SUMMARY

DATE: 02/22/2001

PATENT APPLICATION: US/09/068,377A

TIME: 10:34:24

Input Set : A:\PTO.txt

Output Set: N:\CRF3\02222001\I068377A.raw

L:616 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:26
L:616 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:617 M:252 E: No. of Seq. differs, <211>LENGTH:Input:907 Found:500 SEQ:26
L:619 M:216 E: (34) Seq.#s missing, SEQ ID NOS: 27 thru 32
L:631 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:33 differs:34
L:634 M:214 E: (33) Seq.# missing, SEQ ID NO:34
L:640 M:282 W: Numeric Field Identifier Missing, <212> is required.
L:640 M:282 W: Numeric Field Identifier Missing, <213> is required.
L:640 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:35 differs:37
L:643 M:216 E: (34) Seq.#s missing, SEQ ID NOS: 36 thru 37
L:645 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:650 M:280 W: Numeric Identifier already exists, Length not replaced.
L:651 M:280 W: Numeric Identifier already exists, Type not replaced.
L:657 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:39 differs:37
L:661 M:216 E: (34) Seq.#s missing, SEQ ID NOS: 40 thru 41
L:674 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:42 differs:43
L:675 M:252 E: No. of Seq. differs, <211>LENGTH:Input:47 Found:29 SEQ:42
L:677 M:214 E: (33) Seq.# missing, SEQ ID NO:43
L:682 M:282 W: Numeric Field Identifier Missing, <212> is required.
L:682 M:282 W: Numeric Field Identifier Missing, <213> is required.
L:682 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:44 differs:46
L:685 M:216 E: (34) Seq.#s missing, SEQ ID NOS: 45 thru 46
L:688 M:201 W: Mandatory field data missing, ORGANISM
L:691 M:280 W: Numeric Identifier already exists, Length not replaced.
L:692 M:280 W: Numeric Identifier already exists, Type not replaced.
L:693 M:280 W: Numeric Identifier already exists, Organism not replaced.
L:698 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:47 differs:48
L:699 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:10 SEQ:47
L:700 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:701 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:48
L:701 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:701 M:252 E: No. of Seq. differs, <211>LENGTH:Input:34 Found:10 SEQ:47
L:707 M:282 W: Numeric Field Identifier Missing, <210> is required.
L:707 M:282 W: Numeric Field Identifier Missing, <211> is required.
L:707 M:282 W: Numeric Field Identifier Missing, <212> is required.
L:707 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:47 differs:51
L:713 M:216 E: (34) Seq.#s missing, SEQ ID NOS: 48 thru 52
L:724 M:216 E: (34) Seq.#s missing, SEQ ID NOS: 54 thru 55
L:725 M:280 W: Numeric Identifier already exists, Length not replaced.
L:726 M:280 W: Numeric Identifier already exists, Type not replaced.
L:727 M:280 W: Numeric Identifier already exists, Organism not replaced.
L:730 M:250 E: Invalid Numeric Identifier, INVALID IDENTIFIER
L:736 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:56 differs:57
L:739 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:740 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:740 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
L:740 M:252 E: No. of Seq. differs, <211>LENGTH:Input:42 Found:37 SEQ:53
L:745 M:282 W: Numeric Field Identifier Missing, <210> is required.

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L:745 M:282 W: Numeric Field Identifier Missing, <211> is required.
L:745 M:282 W: Numeric Field Identifier Missing, <212> is required.
L:745 M:282 W: Numeric Field Identifier Missing, <213> is required.
L:745 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:56 differs:60
L:748 M:216 E: (34) Seq.#s missing, SEQ ID NOS: 57 thru 60
L:750 M:250 E: Invalid Numeric Identifier, INVALID IDENTIFIER
L:754 M:280 W: Numeric Identifier already exists, Length not replaced.
L:763 M:280 W: Numeric Identifier already exists, Organism not replaced.
L:768 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:62 differs:65
L:770 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:771 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:65
L:771 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:4
L:772 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:65
L:772 M:252 E: No. of Seq. differs, <211>LENGTH:Input:41 Found:30 SEQ:61
L:774 M:216 E: (34) Seq.#s missing, SEQ ID NOS: 63 thru 66
L:784 M:216 E: (34) Seq.#s missing, SEQ ID NOS: 68 thru 69
L:785 M:280 W: Numeric Identifier already exists, Length not replaced.
L:786 M:280 W: Numeric Identifier already exists, Type not replaced.
L:787 M:280 W: Numeric Identifier already exists, Organism not replaced.
L:792 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:70 differs:65
L:793 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:794 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:794 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:794 M:252 E: No. of Seq. differs, <211>LENGTH:Input:33 Found:0 SEQ:67
L:796 M:282 W: Numeric Field Identifier Missing, <210> is required.
L:796 M:282 W: Numeric Field Identifier Missing, <211> is required.
L:796 M:282 W: Numeric Field Identifier Missing, <212> is required.
L:796 M:282 W: Numeric Field Identifier Missing, <213> is required.
L:796 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:70 differs:71
L:799 M:214 E: (33) Seq.# missing, SEQ ID NO:71
L:818 M:280 W: Numeric Identifier already exists, <130> found multiple times
L:818 M:281 W: Numeric Fields not Ordered, <130> not ordered!.
L:820 M:280 W: Numeric Identifier already exists, <140> found multiple times
L:820 M:281 W: Numeric Fields not Ordered, <140> not ordered!.
L:821 M:280 W: Numeric Identifier already exists, <141> found multiple times
L:821 M:281 W: Numeric Fields not Ordered, <141> not ordered!.
L:823 M:281 W: Numeric Fields not Ordered, <150> not ordered!.
L:830 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:830 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:831 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:831 M:254 E: No. of Bases conflict, LENGTH:Input:85 Counted:48 SEQ:72
L:831 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:48
M:254 Repeated in SeqNo=72
L:836 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:836 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:837 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:837 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:48
L:841 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:842 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1

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L:843 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:843 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:48
L:847 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:848 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:849 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:849 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:48
L:852 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:853 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:854 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:854 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:48
L:857 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:858 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:859 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:859 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:50
L:862 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:863 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:864 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:864 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:48
L:867 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:868 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:868 M:252 E: No. of Seq. differs, <211>LENGTH:Input:31 Found:338 SEQ:72
L:869 M:280 W: Numeric Identifier already exists, Organism not replaced.
L:871 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:72 differs:2
L:875 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:876 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:876 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:50
L:881 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:882 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:882 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:54
L:887 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:888 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:888 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:51
L:893 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:894 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:894 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:55
L:899 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:900 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:900 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:57
L:905 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:906 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:906 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:57
L:911 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:912 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:912 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:57
L:917 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:918 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:918 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:919 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:921 M:252 E: No. of Seq. differs, <211>LENGTH:Input:31 Found:1115 SEQ:72

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L:932 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:933 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:933 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
M:332 Repeated in SeqNo=4
L:934 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:934 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:939 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:939 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:940 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:940 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:941 M:252 E: No. of Seq. differs, <211>LENGTH:Input:50 Found:30 SEQ:4
L:943 M:214 E: (33) Seq.# missing, SEQ ID NO:5
L:944 M:280 W: Numeric Identifier already exists, Length not replaced.
L:945 M:280 W: Numeric Identifier already exists, Type not replaced.
L:946 M:280 W: Numeric Identifier already exists, Organism not replaced.
L:950 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:950 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:950 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:950 M:252 E: No. of Seq. differs, <211>LENGTH:Input:50 Found:10 SEQ:4
L:958 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:7
L:959 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:959 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
M:332 Repeated in SeqNo=7
L:965 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:965 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:966 M:252 E: No. of Seq. differs, <211>LENGTH:Input:48 Found:30 SEQ:7
L:968 M:216 E: (34) Seq.#s missing, SEQ ID NOS: 8 thru 9
L:976 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:10 differs:7
L:977 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:978 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:978 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:3
L:979 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:979 M:252 E: No. of Seq. differs, <211>LENGTH:Input:45 Found:0 SEQ:10
L:981 M:282 W: Numeric Field Identifier Missing, <210> is required.
L:981 M:282 W: Numeric Field Identifier Missing, <211> is required.
L:981 M:282 W: Numeric Field Identifier Missing, <212> is required.
L:981 M:282 W: Numeric Field Identifier Missing, <213> is required.
L:981 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:10 differs:11
L:984 M:214 E: (33) Seq.# missing, SEQ ID NO:11
L:991 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:12 differs:14
L:992 M:252 E: No. of Seq. differs, <211>LENGTH:Input:36 Found:17 SEQ:12
L:994 M:216 E: (34) Seq.#s missing, SEQ ID NOS: 13 thru 14
L:1007 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:15 differs:16
L:1008 M:252 E: No. of Seq. differs, <211>LENGTH:Input:41 Found:37 SEQ:15
L:1010 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:1014 M:282 W: Numeric Field Identifier Missing, <211> is required.
L:1014 M:282 W: Numeric Field Identifier Missing, <212> is required.
L:1014 M:282 W: Numeric Field Identifier Missing, <213> is required.
L:1014 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:19

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L:1020 M:201 W: Mandatory field data missing, ORGANISM
L:1026 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:1026 M:252 E: No. of Seq. differs, <211>LENGTH:Input:20 Found:5 SEQ:20
L:1029 M:280 W: Numeric Identifier already exists, Length not replaced.
L:1030 M:250 E: Invalid Numeric Identifier, INVALID IDENTIFIER
L:1044 M:280 W: Numeric Identifier already exists, Organism not replaced.
L:1046 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:21 differs:26
L:1048 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:1049 M:333 E: Wrong sequence grouping, Amino acids not in groups!
M:332 Repeated in SeqNo=21
L:1055 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:1055 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:1060 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:1060 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:1065 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:1065 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:1070 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:1070 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:1075 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:1075 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:1080 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:1080 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:1085 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:1086 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:1086 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:1091 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:1092 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:1092 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:1097 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:1098 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:1098 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:1099 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:1099 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:1100 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:1100 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:1101 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:1101 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:1102 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:1102 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:1103 M:342 E: Invalid Stop Code On Error, STOP CODON:*
L:1103 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:1103 M:252 E: No. of Seq. differs, <211>LENGTH:Input:20 Found:151 SEQ:20
L:23 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (73) Counted (47)